

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 27, 2005, 20:54:04 ; Search time 126 Seconds
(without alignments)

11058.472 Million cell updates/sec

Title: us-10-038-854-38

Perfect score: 14495
Sequence: 1 MDVKERRPYCSLTLSRRREKRE.....ELADSNANIQPLROSEIGRR 2721

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: UniProt_03.*
1: uniProt_sprot.*
2: uniProt_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14248	98.3	2715	2 Q9WTS6	Q9WTS6 mus musculu
2	12351	85.2	2346	2 Q9JLC1	Q9JLC1 mus musculu
3	11627	80.2	2590	2 Q9W7R4	Q9W7R4 brachydanio
4	10403	71.8	2765	2 Q9RIK2	Q9RIK2 rattus norv
5	10393.5	71.7	2802	2 Q9DERS	Q9DERS gallus gall
6	10393.5	71.7	2764	2 Q9WTS5	Q9WTS5 mus musculu
7	10189	70.3	2771	2 Q9WTS7	Q9WTS7 mus musculu
8	9764.5	69.0	2825	2 Q70465	Q70465 mus musculu
9	9764.5	67.4	2824	2 Q9W7R3	Q9W7R3 brachydanio
10	9489	65.5	1828	2 Q80TJ2	Q80TJ2 mus musculu
11	9267	63.9	1769	2 Q9W6T6	Q9W6T6 gallus gall
12	9035	62.3	2705	2 Q9W6T6	Q9W6T6 gallus gall
13	8972	61.9	2731	2 Q9WTS4	Q9WTS4 mus musculu
14	8884	61.3	2725	2 Q9JLC2	Q9JLC2 homo sapien
15	8463.5	58.4	2144	2 Q9ULR2	Q9ULR2 homo sapien
16	8368	57.7	2192	2 Q804R1	Q804R1 brachydanio
17	5447	37.6	1045	2 Q9NW11	Q9NW11 homo sapien
18	5313	36.7	1399	2 Q6N022	Q6N022 homo sapien
19	5040	34.8	964	2 Q9NV77	Q9NV77 homo sapien
20	4470.5	30.8	1198	2 Q80TJ5	Q80TJ5 mus musculu
21	4061.5	28.0	1086	2 Q9P2P4	Q9P2P4 homo sapien
22	4037.5	27.9	1071	2 Q723C7	Q723C7 homo sapien
23	3930.5	27.1	2633	2 Q70XK2	Q70XK2 anopheles g
24	3847	26.5	2731	2 Q6L307	Q6L307 drosophila
25	3847	26.5	2731	2 Q9VNU6	Q9VNU6 drosophila
26	3839	26.5	2515	2 Q24551	Q24551 drosophila
27	3839	26.5	2731	2 Q18366	Q18366 drosophila
28	3571.5	24.6	3004	2 Q24550	Q24550 drosophila
29	3569.5	24.6	3004	2 Q9VYN8	Q9VYN8 drosophila
30	3520.5	24.3	2754	2 Q7PRV4	Q7PRV4 anopheles g
31	3489.5	24.1	930	2 Q9JLCO	Q9JLCO mus musculu

32	3416	23.6	991	2 Q8CAT1	Q8CAT1 mus musculu
33	3283	22.6	625	2 Q96SY2	Q96SY2 homo sapien
34	3213.5	22.2	849	2 Q9WTS6	Q9WTS6 homo sapien
35	2809	19.4	730	2 Q9WTS6	Q9WTS6 homo sapien
36	2784	19.2	831	2 Q9PU49	Q9PU49 gallus gall
37	2316	16.0	442	2 Q9NZJ2	Q9NZJ2 homo sapien
38	2237	15.4	2560	2 Q21980	Q21980 caenorhabdi
39	2198.5	15.2	2531	2 Q8MP22	Q8MP22 caenorhabdi
40	1673.5	11.5	339	2 Q8BSL5	Q8BSL5 mus musculu
41	1531	10.6	372	2 Q9RIK0	Q9RIK0 rattus norv
42	1178.5	8.1	272	2 Q9RIJ9	Q9RIJ9 rattus norv
43	1155.5	8.0	266	2 Q9RIK1	Q9RIK1 rattus norv
44	1154	8.0	229	2 Q9QVZ1	Q9QVZ1 mus musculu
45	1096	7.6	536	2 Q8C8D2	Q8C8D2 mus musculu

ALIGNMENTS

RESULT 1

ID	Q9WTS6	PRELIMINARY;	PRT;	2715 AA.
AC	Q9WTS6;			
DT	01-NOV-1999 (TrEMBLrel. 12, Created)			
DT	01-NOV-1999 (TrEMBLrel. 12, Last sequence update)			
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DE	Ten-m3.			
GN	Name=Od23; Synonyms=ten-m3;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
FM	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Balb/c; TISSUE=Brain;			
RA	Ochoaishi T., Zhou X., Peng K., Richter B., Moergelin M., Perez M.T.,			
RA	Su W., Chiquet-Ehrismann R., Rauch U., Passler R.;			
RT	"Mouse Ten-m/Od2 is a new family of dimeric type II transmembrane			
RT	proteins expressed in many tissues.";			
RL	J. Cell Biol. 0:0-0(1999).			
CC	-1- SIMILARITY: Contains 8 EGF-like domains.			
DR	EMBL; AB025412; BAB7398.1; -.			
DR	HSSP; P00750; ITPG.			
DR	MED; MG1:1345183; Od23.			
DR	InterPro; IPR011044; Amino_DH_B_like.			
DR	InterPro; IPR000742; EGF_2.			
DR	InterPro; IPR006209; EGF-like.			
DR	InterPro; IPR006210; IEGF.			
DR	InterPro; IPR001258; NHL.			
DR	InterPro; IPR009041; FMP_SGCT.			
DR	InterPro; IPR009471; Ten_N.			
DR	InterPro; IPR006530; YD.			
DR	Pfam; PF00008; EGF_3.			
DR	Pfam; PF01436; NHL_6.			
DR	Pfam; PF05593; RKS_repeat; 6.			
DR	Pfam; PF06484; Ten_N_1.			
DR	SMART; SM00181; EGF_7.			
DR	TIGRFAMs; TIGR01643; YD_repeat_2x; 5.			
DR	PROSITE; PS00023; EGF_1; 8.			
DR	PROSITE; PS01186; EGF_2; 7.			
DR	PROSITE; PS50026; EGF_3; 3.			
KW	EGF-like domain.			
SQ	SEQUENCE 2715 AA; 303063 MW; 598F46A7734C2B1 CRC64;			
Query Match	98.3%;	Score 14248;	DB 2;	Length 2715;
Best Local Similarity	97.9%;	Pred. No. 0;		
Matches 2664;	Conservative 33;	Mismatches 18;	Indels 6;	Gaps 1;
QY	1 MDVKERRPYCSLTLSRRREKRRYTNSSADNIEGCRVPTQKSYSSSELTAKFDHDSRLLYG 60			
DB	1 MDVKERRPYCSLTLSRRREKRRYTNSSADNIEGCRVPTQKSYSSSELTAKFDHDSRLLYG 60			
QY	61 NRYVDLVHREADFTTQGNFTLRQLGVCPEATRRGLAFCAEWGLPHRGYSISAGSDADT 120			

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OM protein - protein search, using sw model

Run on: September 27, 2005, 20:56:29 ; Search time 32 Seconds

(without alignments)
8181.432 Million cell updates/sec

Title: US-10-038-854-38

Perfect score: 1495
Sequence: 1 MDVKKRRPYCSLTYSRRREKE.....ELADSNANIQLRQSEIGRR 2721

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	10001	69.0	2825 2	T14271 Doc4 protein, stre
2	3839	26.5	2515 2	S47008 tenascin-like prot
3	3534	24.4	2406 2	AS4148 odz protein - fruit
4	3213.5	22.2	849 2	T46253 hypothetical prote
5	2226.5	15.4	2531 2	T16743 hypothetical prote
6	1184.5	8.2	782 2	A61625 tenascin-like prot
7	703	4.8	2019 1	J01332 tenascin precursor
8	699	4.8	2201 2	A32160 tenascin-C - human
9	689	4.8	184 2	T12457 hypothetical prote
10	680.5	4.7	1746 1	S19634 tenascin precursor
11	659.5	4.5	1810 1	A32260 tenascin precursor
12	637	4.4	4006 2	T09070 probable tenascin
13	616	4.2	3566 1	A40701 tenascin-X precurs
14	590	4.1	4135 2	T42629 tenascin-X - bovin
15	589	4.1	647 2	A43902 tenascin - eastern
16	472.5	3.3	1620 2	T27283 hypothetical prote
17	455.5	3.1	1203 2	A49175 Notch B protein -
18	455.5	3.1	2471 2	A49128 cell-fate determin
19	448.5	3.1	3191 2	T22945 hypothetical prote
20	427.5	2.9	2703 1	A24420 notch protein - fr
21	424.5	2.9	2555 2	A40043 notch protein homo
22	421.5	2.9	2531 1	JH0675 restrictin precurs
23	419	2.9	2531 2	S18188 notch protein homo
24	419	2.9	2531 2	A46019 notch-1 protein -
25	417.5	2.9	1064 2	A40136 fibropellin Ia - s
26	417.5	2.9	1111 2	T26972 hypothetical prote
27	417.5	2.9	1220 2	A56136 jagged protein pre
28	417.5	2.9	2321 2	S78549 notch protein - h
29	416.5	2.9	2318 2	S45306 notch 3 protein -

30	414.5	2.9	1356 2	A45445 janusin precursor,
31	413.5	2.9	1574 2	T13954 MEGR protein - ra
32	402.5	2.8	2437 2	S42612 transmembrane prot
33	402.5	2.8	2524 2	A35844 Notch protein - Af
34	389.5	2.7	473 2	A56175 adhesive plaque pr
35	388.5	2.7	1964 2	T09059 notch4 - mouse
36	388	2.7	1408 2	S16148 gene secrete prote
37	385.5	2.7	2139 2	A35672 crumbs protein - f
38	384.5	2.7	1732 2	E89753 protein Flt7.4 (1
39	384	2.6	2531 2	T31070 notch homolog prot
40	382	2.6	2352 2	T30201 Notch homolog prot
41	377.5	2.6	1295 2	A32901 glp1 protein precu
42	370	2.6	2334 2	S32920 cell wall associat
43	365	2.5	1429 2	S06434 homeotic protein 1
44	360.5	2.5	832 2	A31246 neurogenic protein
45	360.5	2.5	880 2	S00670 neurogenic repetit

ALIGNMENTS

RESULT 1
T14271
Doc4 protein, stress-induced - mouse
N/Alternate names: odz protein homolog
C/Species: Mus musculus (house mouse)
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T14271
R/Mang, X.Z.; Kuroda, M.; Sok, J.; Batchvarova, N.; Kimmel, R.; Chung, P.; Zluzner, H.
EMBL J. 17 3619-3630, 1998
A/Title: Identification of novel stress-induced genes downstream of chop.
A/Reference number: Z17951; MUID:98315054; PMID:9649432
A/Accession: T14271
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-2825 <MAN>
A/Cross-references: UNIPROT:O70465; EMBL:AF059485; NID:g3170614; PID:g3170615; PIDN:AAC
A/Genetics:
A/Gene: Doc4

QY	Query Match	69.0%	Score 10001;	DB 2;	Length 2825;
DB	Best Local Similarity	64.6%	Best. No. 0;		
	Matches 1850;	Conservative 364;	Mismatches 469;	Indels 180;	Gaps 23;
QY	1	MDVKKRRPYCSLTYSRRREKERYTNSADNBEGRVPTOKSYSSSEITLAKADHDSRLLYG	60		
DB	1	MDVKKRRPYCSLTYSRRREKERYTNSADNBEGRVPTOKSYSSSEITLAKADHDSRLLYG	57		
QY	61	NRVADLVHREADEPFTQGNFTLRQLGVCCEPATRRGLAFCAMGLPHRGYSISASDADT	120		
DB	58	SRVADWVPQAEFEFCRTGNTFTLRQLGVCCEPATRRGLAFCAMGLPHRGYSISASDADT	117		
QY	121	ENRANVSPHMANLNGRGVSGSSCLSSRSNSALTTDREHN	164		
DB	118	EADTVLSPHPRVLMGRSTRSGSSCLSSRSNSALTTDREHN	177		
QY	165	-----KDSR-----	NEOP 173		
DB	178	IEGSPSPPPPPANESGRRLGNGVAPTPDSDSEEFVNSPLVKSASLGVAAANDHP	237		
QY	174	ASNGOGSTIQ-----PLPSSHQKSAOH-PSITSLNNSLITNRNOSPAP	PA 220		
DB	238	SSIQNHPRLRTPPPPLPHATPN--QHHAASINSLNKGNFTPRSNPAPATDLSLGEPP	295		
QY	221	ALPAELQTPRESVQLQDSWTLGNNVLESF-----	250		
DB	296	AGSAQ-----EPHQAQDNWVANSKIPETENLAKOPFLGTWQDNLLEMDIFASRRDGAY	350		
QY	251	---HPLFKTGTTGTPPLFSTATPGYTASGVSPPTPLPRNTLSASAPFKTSKXCSW	307		
DB	351	SDGHFFPKRG-GTSPLFCITTSFGYPLTSSVYVPPPRPLPRSFSPAPPLKXPSKCNW	409		
QY	308	KCTALCAVGSVLAAILLSYFIAMHLFGLNWLOQQTENDTFENGKVNSDT-----MPTNT	362		

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OM protein - protein search, using sw model

Run on: September 27, 2005, 21:02:29 ; Search time 114 Seconds
(without alignments)
9715.053 Million cell updates/sec

Title: US-10-038-854-38
Perfect score: 14495
Sequence: 1 MDVKEKRRPYCSLTYSRREKE.....ELADSNNTQFLROSGIGRR 2721

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1826554 seqs, 407025358 residues
Total number of hits satisfying chosen parameters: 1826554

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubppaa/PCR_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubppaa/PCITUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubppaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubppaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubppaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubppaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubppaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubppaa/US10E_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubppaa/US11A_PUBCOMB.pep:*
20: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14495	100.0	2721	15	US-10-038-854-38
2	14475	99.9	2725	15	US-10-038-854-36
3	14248	98.3	2715	15	US-10-042-865-52
4	14248	98.3	2715	15	US-10-029-020-51
5	13944.5	96.2	2628	15	US-10-038-854-40
6	13834	95.4	2613	15	US-10-038-854-42
7	13351	85.4	2346	15	US-10-072-012-491
8	11627	80.2	2590	15	US-10-072-012-490
9	10403	71.8	2765	9	US-09-808-602-84
10	10403	71.8	2765	10	US-09-800-198-72
11	10403	71.8	2765	15	US-10-072-012-488

12	10394.5	71.7	2802	9	US-09-808-602-81	Sequence 81, Appl
13	10394.5	71.7	2802	10	US-09-800-198-69	Sequence 69, Appl
14	10394.5	71.7	2802	15	US-10-072-012-489	Sequence 489, App
15	10394	71.7	2759	15	US-10-072-012-144	Sequence 144, App
16	10393.5	71.7	2764	9	US-09-808-602-80	Sequence 80, Appl
17	10393.5	71.7	2764	9	US-09-808-602-80	Sequence 68, Appl
18	10393.5	71.7	2764	15	US-10-072-012-487	Sequence 487, App
19	10347.5	71.4	2794	15	US-10-042-865-2	Sequence 2, Appl
20	10310.5	71.1	2724	9	US-09-808-602-13	Sequence 13, Appl
21	10310.5	71.1	2724	10	US-09-800-198-13	Sequence 13, Appl
22	10309	71.1	2733	9	US-09-808-602-8	Sequence 8, Appl
23	10309	71.1	2733	10	US-09-800-198-8	Sequence 8, Appl
24	10221	70.5	2769	15	US-10-029-020-14	Sequence 14, Appl
25	10221	70.5	2769	15	US-10-029-020-14	Sequence 82, Appl
26	10189	70.3	2771	9	US-09-808-602-82	Sequence 82, Appl
27	10189	70.3	2771	10	US-09-800-198-70	Sequence 70, Appl
28	10144.5	70.0	2758	18	US-10-467-535-10	Sequence 10, Appl
29	10078	69.5	2633	15	US-10-144-194A-82	Sequence 82, Appl
30	10078	69.5	2633	16	US-10-491-566-82	Sequence 82, Appl
31	10010	69.1	2775	15	US-10-383-201-56	Sequence 56, Appl
32	9491	65.5	2551	15	US-10-144-194A-80	Sequence 80, Appl
33	9491	65.5	2551	16	US-10-491-566-80	Sequence 80, Appl
34	9267	63.9	1769	16	US-10-723-860-4494	Sequence 4494, Ap
35	8964	61.8	2725	15	US-10-029-020-52	Sequence 52, Appl
36	8964	61.8	2725	16	US-10-408-765A-1687	Sequence 1687, Ap
37	8884	61.3	2725	15	US-10-295-027-928	Sequence 928, App
38	8884	61.3	2725	16	US-10-723-860-4102	Sequence 4102, Ap
39	8463.5	58.4	2144	16	US-10-723-860-2303	Sequence 2303, Ap
40	6702.5	46.2	1737	9	US-09-808-602-83	Sequence 83, Appl
41	6702.5	46.2	1737	10	US-09-800-198-71	Sequence 71, Appl
42	6523.5	45.0	1688	15	US-10-144-194A-113	Sequence 113, App
43	6523.5	45.0	1688	16	US-10-491-566-113	Sequence 113, App
44	6523.5	45.0	1688	17	US-10-494-940-52	Sequence 52, Appl
45	5447	37.6	1045	15	US-10-042-865-54	Sequence 54, Appl

ALIGNMENTS

RESULT 1
US-10-038-854-38
; Sequence 38, Application US/10038854
; Publication No. US20040022781A1
; GENERAL INFORMATION:
; APPLICANT: SPYTEK, Kimberly A
; APPLICANT: Li, Li
; APPLICANT: Wolenc, Adam R
; APPLICANT: Verne, Corine
; APPLICANT: Eisen, Andrew J
; APPLICANT: Liu, Xiaohong
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shinkets, Richard A
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spaderne, Steven K
; APPLICANT: Gorman, Linda
; APPLICANT: Paturajan, Ramesh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Gangoli, Beba A
; APPLICANT: Guo, Xiaojia S
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Rastelli, Luca
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Bugees, Catherine E
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Eilerman, Karen
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: MacDougall, John R
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-230

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OM protein - protein search, using sw model

Run on: September 27, 2005, 20:57:04 ; Search time 32 Seconds
(without alignment)
6347.503 Million cell updates/sec

Title: US-10-038-854-38
Perfect score: 14495
Sequence: 1 MDVYERPPYSLTFSRREKE.....ELADSNANIQFLNROSEIGRR 2721

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1485	10.2	560	3 US-08-891-845-4	Sequence 4, Appli
2	1485	10.2	560	4 US-09-514-573-4	Sequence 4, Appli
3	1485	10.2	768	4 US-08-891-845-2	Sequence 2, Appli
4	1485	10.2	768	4 US-09-514-573-2	Sequence 2, Appli
5	839.5	5.8	501	3 US-08-891-845-10	Sequence 10, Appli
6	839.5	5.8	501	4 US-09-514-573-10	Sequence 10, Appli
7	639.5	4.8	2200	4 US-09-796-575-2	Sequence 2, Appli
8	687.5	4.7	2199	4 US-08-793-273C-2	Sequence 2, Appli
9	687.5	4.7	2199	5 PCT-US95-11684-2	Sequence 2, Appli
10	659.5	4.5	1810	4 US-08-793-273C-4	Sequence 4, Appli
11	659.5	4.5	1810	5 PCT-US95-11684-4	Sequence 4, Appli
12	615	4.2	2254	4 US-09-949-016-9270	Sequence 9270, Ap
13	446.5	3.1	2471	1 US-08-185-432-16	Sequence 16, Appli
14	446.5	3.1	2471	1 US-08-083-590A-19	Sequence 19, Appli
15	446.5	3.1	2471	4 US-08-533-384-19	Sequence 19, Appli
16	446.5	3.1	2471	4 US-08-899-232-1	Sequence 1, Appli
17	446.5	3.1	2471	4 US-09-121-457-1	Sequence 1, Appli
18	446.5	3.0	2703	1 US-08-185-432-19	Sequence 19, Appli
19	428.5	3.0	2703	1 US-08-899-232-4	Sequence 4, Appli
20	428.5	3.0	2703	4 US-09-121-457-4	Sequence 4, Appli
21	426	2.9	1193	2 US-08-400-159-10	Sequence 10, Appli
22	426	2.9	1193	3 US-08-611-729A-10	Sequence 10, Appli
23	426	2.9	1193	4 US-09-195-524-10	Sequence 10, Appli
24	418.5	2.9	1010	3 US-08-882-046-7	Sequence 7, Appli
25	418.5	2.9	1010	4 US-09-566-047-6	Sequence 6, Appli
26	418.5	2.9	1036	3 US-09-068-740A-6	Sequence 7, Appli
27	418.5	2.9	1067	4 US-09-579-536C-18	Sequence 18, Appli

28	418.5	2.9	1187	3 US-09-068-740A-7	Sequence 7, Appli
29	418.5	2.9	1208	4 US-09-199-865-1	Sequence 1, Appli
30	418.5	2.9	1208	4 US-10-213-329-1	Sequence 1, Appli
31	418.5	2.9	1218	2 US-08-400-159-6	Sequence 6, Appli
32	418.5	2.9	1218	3 US-08-611-729A-6	Sequence 6, Appli
33	418.5	2.9	1218	3 US-08-882-046-2	Sequence 2, Appli
34	418.5	2.9	1218	3 US-09-068-740A-11	Sequence 11, Appli
35	418.5	2.9	1218	4 US-09-566-047-2	Sequence 2, Appli
36	418.5	2.9	1218	4 US-09-917-254-85	Sequence 85, Appli
37	418.5	2.9	1218	4 US-09-195-524-6	Sequence 6, Appli
38	418.5	2.9	1218	4 US-09-579-536C-1	Sequence 1, Appli
39	418.5	2.9	1218	4 US-09-949-016-5902	Sequence 5902, Ap
40	418.5	2.9	1234	4 US-09-949-016-10297	Sequence 10297, A
41	417.5	2.9	1219	3 US-08-882-046-5	Sequence 5, Appli
42	417.5	2.9	1219	4 US-09-566-047-5	Sequence 5, Appli
43	417.5	2.9	2321	4 US-09-230-652-2	Sequence 2, Appli
44	415	2.9	1055	3 US-09-214-278-2	Sequence 2, Appli
45	415	2.9	1055	4 US-09-855-722-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-891-845-4
Sequence 4, Application US/08891845
Patent No. 6096873
GENERAL INFORMATION:
APPLICANT: Schaefer, Gabriele M.
APPLICANT: Sliwowski, Mark
TITLE OF INVENTION: Gamma-Herregulin
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/891,845
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/021640
FILING DATE: 07/12/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1043
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 560 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-891-845-4
Query Match 10.2%; Score 1485; DB 3; Length 560;
Best Local Similarity 54.1%; Pred. No. 1.5e-103;
Matches 311; Conservative 62; Mismatches 124; Indels 78; Gaps 13;
CY 1 MDVYERPPYSLTFSRREKRRRTYNSGADNBECKVPTOKYSSSETTKAPHDSSRLTYG 60
DB 1 MDVYERPPYSLTFR-RDADRRYTTSSADSBEGKAP-OKSYSSSETTKAYDQD-ARLAYG 57

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OM protein - protein search, using sw model

Run on: September 27, 2005, 20:53:38 ; Search time 111 Seconds
(without alignments)
9480.856 Million cell updates/sec

Title: US-10-038-854-38

Perfect score: 14495
Sequence: 1 MDVRRRPPYCSLTYSRRKE.....ELADSNANNIOFROSEIGRR 2721

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : λ Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003s:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14495	100.0	2721	5	ABP53587 Human NOV
2	14495	100.0	2721	8	ADH41969 Human NOV
3	14475	99.9	2725	5	ABP53586 Human NOV
4	14475	99.9	2725	8	ADH41995 Human NOV
5	14475	99.9	2725	8	ADH41991 Human NOV
6	14475	99.9	2725	8	ADH41933 Human NOV
7	14475	99.9	2725	8	ADH41997 Human NOV
8	14475	99.9	2725	8	ADH41999 Human NOV
9	14475	99.9	2725	8	ADH41973 Human NOV
10	14470	99.8	2725	8	ADH41993 Human NOV
11	13944.5	96.2	2628	5	ABP53588 Human NOV
12	13944.5	96.2	2628	8	ADH41949 Human NOV
13	13834	95.4	2613	5	ABP53589 Human NOV
14	13834	95.4	2613	8	ADH41977 Human NOV
15	12351	85.2	2346	5	ADH16955 Murine NO
16	11627	80.2	2590	5	ADH16954 Zebrafish
17	10417	71.9	2765	8	ADH71220 Human pro
18	10403	71.8	2765	8	ADH16952 Rat NOV
19	10394.5	71.7	2802	5	ADH16953 Chicken N
20	10394	71.7	2759	5	ADH16608 Human NOV
21	10394	71.7	2759	8	ADH71272 Human pro
22	10393.5	71.7	2764	5	ADH16951 Murine NO
23	10393.5	71.7	2764	8	ADH76262 Marker ge
24	10347.5	71.4	2794	8	ABP58401 Human NOV
25	10310.5	71.1	2724	4	AAU08681 Human FCT

26	10310.5	71.1	2724	7	ADH32029 Human pro
27	10310.5	71.1	2724	8	ADH71252 Human pro
28	10309	71.1	2733	4	AAU08680 Human FCT
29	10309	71.1	2733	8	ADH71250 Human pro
30	10309	71.1	2733	8	ADH71254 Human pro
31	10309	71.1	2733	8	ADH71240 Human pro
32	10309	71.1	2733	8	ADH71246 Human pro
33	10309	71.1	2733	8	ADH71258 Human pro
34	10307	71.1	2733	7	ADH32024 Human FCT
35	10221	70.5	2769	5	ABG70388 Human TEN
36	10221	70.5	2769	7	ADP74830 Human NO
37	10144.5	70.0	2758	5	ABG97359 Human CGD
38	10078	69.5	2633	6	ABP58318 Human NOV
39	10051	69.3	2769	8	ADN42262 Human nov
40	10010	69.1	2775	7	ADP74842 Murine NO
41	9933.5	68.5	2662	8	ADH71218 Human pro
42	9491	65.5	2551	6	ABP58317 BCUD205A
43	9267	63.9	1769	8	ADQ21674 Human sof
44	9232	63.7	2333	8	ADH71274 Human pro
45	8964	61.8	2725	7	ADH69881 Human hea

ALIGNMENTS

RESULT 1	ABP53587	standard; protein; 2721 AA.
XX	ABP53587	
AC	ABP53587	
DT	17-DEC-2002	(first entry)
XX		
DE	Human NOV15b protein SEQ ID NO:38.	
XX		
KM	Human, NOV; cytosolic; neuroprotective; anticonvulsant; cardiovascular; cerebroprotective; nootropic; antidiabetic; antiinflammatory; fungicide; antifungal; antitubercular; antiparasitic; immunosuppressive; antiviral; anticancer; leukemic; antibacterial; protozoacide; antihelminthic; gene therapy; cancer; leukemia; lymphoma; melanoma; neurological disorder; epilepsy; stroke; ischemic cerebrovascular disease; Alzheimer's disease; allergy; Pick's disease; vesicular transport disease; cystic fibrosis; goitre; diabetes mellitus; Grave's disease; gastrointestinal disorder; vaccine; ulcerative colitis; gastric disorder; duodenal disorder; infection; autoimmune disease; allergic reaction; autoimmune haemolytic anaemia; rheumatoid arthritis; chromosome 4.	
KW		
OS	Homo sapiens.	
XX		
PN	WO200262999-A2.	
XX		
PD	15-AUG-2002.	
XX		
PF	31-DEC-2001; 2001WO-US049976.	
XX		
PR	29-DEC-2000; 2000US-0258928P.	
PR	02-JAN-2001; 2001US-0259415P.	
PR	04-JAN-2001; 2001US-0259785P.	
PR	20-FEB-2001; 2001US-0269814P.	
PR	09-MAR-2001; 2001US-0279863P.	
PR	29-MAR-2001; 2001US-0279832P.	
PR	29-MAR-2001; 2001US-0279832P.	
PR	13-APR-2001; 2001US-0283889P.	
PR	18-APR-2001; 2001US-0284447P.	
PR	25-APR-2001; 2001US-0286683P.	
PR	29-MAY-2001; 2001US-0294080P.	
PR	16-AUG-2001; 2001US-0312915P.	
PR	17-AUG-2001; 2001US-0313325P.	
PR	17-SEP-2001; 2001US-0322699P.	
PR	26-NOV-2001; 2001US-0333350P.	
XX		
PA	(CURA-) CURAGEN CORP.	
XX		

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OM nucleic - nucleic search, using sw model

Run on: September 26, 2005, 22:17:44 ; Search time 16507 Seconds
(without alignments)
19934.913 Million cell updates/sec

Title: US-10-038-854-37
Perfect score: 8645
Sequence: 1 ttggccttcggcgccagaaatt.....actgtacttaactaacttta 8645

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5051.2	58.4	5094	AY405420	AY405420 Homo sapi
2	4850	56.1	5069	AY405421	AY405421 Pan trogl
3	3765.8	43.6	5087	AY405422	AY405422 Mus muscu
4	2727.2	31.5	6246	AY413475	AY413475 Homo sapi
5	2350.6	27.2	5970	AY413476	AY413476 Pan trogl
6	1455	16.8	2627	AK050784	AK050784 Mus muscu
7	1269.6	14.7	3190	AY413477	AY413477 Mus muscu
8	1262	14.6	2925	AY413477	AY413477 Mus muscu
9	1222.8	14.1	3038	AK037897	AK037897 Mus muscu
10	940.6	10.9	3760	AK031268	AK031268 Mus muscu
11	806.6	9.3	883	CD628955	CD628955 56079503H
12	803.4	9.3	826	AU119933	AU119933 AU119933
13	801	9.3	826	CD628960	CD628960 56079619H
14	796	9.2	843	AU124680	AU124680 AU124680
15	783.8	9.1	812	AU133387	AU133387 AU133387
16	780.8	9.0	809	AU119743	AU119743 AU119743
17	776	9.0	776	CA777388	CA777388 ip13c06.x
18	775	9.0	868	CA454304	CA454304 AGENCOURT
19	772.8	8.9	865	CK775005	CK775005 963813 MA
20	760	8.8	848	CK773227	CK773227 961842 MA
21	747.2	8.6	795	CD628956	CD628956 56079503J
22	738.4	8.5	798	CD628958	CD628958 56079603H
23	727.2	8.4	861	BE740880	BE740880 601593311
24	724.6	8.4	732	CN391504	CN391504 170005315

25	714.6	8.3	894	5	BU151768	BU151768 AGENCOURT
26	711.6	8.2	776	2	BE741784	BE741784 601593546
27	707.2	8.2	776	1	AU126844	AU126844 AU126844
28	700.4	8.1	916	5	BQ892798	BQ892798 AGENCOURT
29	698.8	8.1	818	6	CD807778	CD807778 UT-M-GMO
30	695.6	8.0	951	5	BU839812	BU839812 AGENCOURT
31	689.9	8.0	909	4	BP980526	BP980526 602304274
32	688	8.0	720	7	CN391496	CN391496 170004240
33	686.4	7.9	712	7	CN391503	CN391503 170004243
34	681.8	7.9	716	7	CN391499	CN391499 170005325
35	675.8	7.8	792	2	BE898900	BE898900 601682313
36	659.4	7.6	681	2	BE382393	BE382393 601297206
37	656.4	7.6	702	4	BM670316	BM670316 UI-E-DWI-
38	655.6	7.6	854	7	CF745232	CF745232 UI-M-GVO-
39	652.6	7.5	834	5	BU610605	BU610605 UI-M-FCO-
40	646	7.5	658	7	CN391493	CN391493 170005321
41	645.2	7.5	687	2	BE898495	BE898495 601681396
42	642.8	7.4	687	6	CA428646	CA428646 UI-H-PH-
43	641.4	7.4	819	5	BQ443891	BQ443891 UI-M-EMO-
44	640	7.4	724	4	BG419748	BG419748 602451992
45	633.4	7.3	641	7	CN391495	CN391495 170006000

ALIGNMENTS

RESULT 1
LOCUS AY405420 5094 bp DNA linear GSS 12-DEC-2003
DEFINITION Homo sapiens HCM2218 gene, VIRUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY405420
VERSION AY405420.1 GI:39761394
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 5094)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Clivello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Snihsy, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
1..5094
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..5094
/locus_tag="HCM2218"
ORIGIN
Query Match 58.4%; Score 5051.2; DB 9; Length 5094;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 5084; Conservative 0; Mismatches 10; Indels 21; Gaps 1;
Gy 2901 GTTACCTGCTGCAATGATGCTGCTCACTTGTATTTAGACATCCCATTT 2960
Db 1 GTTACCTGCTGCAATGATGCTGCTCTCACTTGTATTTAGACATCCCATTT 60

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OM nucleic - nucleic search, using sw model

Run on: September 27, 2005, 05:59:11; Search time 3289 Seconds
(without alignments)
17574.597 Million cell updates/sec

Title: US-10-038-854-37

Perfect score: 8645
Sequence: 1 ttgcgcctcgagccagaattc.....actgtatttaactta 8645

Scoring table: IDENTITY NUC
Gapop 10'-0, Gapext 1.0

Searched: 7400732 seqs, 3343337571 residues

Total number of hits satisfying chosen parameters: 14801464

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/PC1_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/PC1TIS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq.*
21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	8645	100.0	8645	17	US-10-038-854-37
2	8616.6	99.7	8675	17	US-10-038-854-35
3	8000.6	92.5	8473	17	US-10-038-854-39
4	7895.8	91.3	8487	17	US-10-038-854-41
5	5952.8	68.9	6810	20	US-10-723-860-8301
6	5305.8	61.4	5309	20	US-10-723-860-4493
7	3714.8	43.0	8575	18	US-10-072-012-143

8	3614	41.8	3614	17	US-10-172-118-1743	Sequence 1743, Ap
9	3614	41.8	3614	18	US-10-342-887-1743	Sequence 1743, Ap
10	3614	41.8	3614	21	US-10-848-755A-185	Sequence 185, Ap
11	3589.8	41.5	8438	17	US-10-042-865-1	Sequence 1, Appl1
12	3566.6	41.3	8409	9	US-09-808-602-79	Sequence 79, Appl1
13	3566.6	41.3	8409	10	US-09-800-198-67	Sequence 67, Appl1
14	3545.6	41.0	8797	9	US-09-808-602-74	Sequence 74, Appl1
15	3545.6	41.0	8797	9	US-09-808-602-77	Sequence 77, Appl1
16	3545.6	41.0	8797	10	US-09-800-198-62	Sequence 62, Appl1
17	3545.6	41.0	8797	10	US-09-800-198-65	Sequence 65, Appl1
18	3518.4	40.7	8689	9	US-09-808-602-78	Sequence 78, Appl1
19	3518.4	40.7	8689	10	US-09-800-198-66	Sequence 66, Appl1
20	3502.2	40.5	8354	17	US-10-383-201-43	Sequence 43, Appl1
21	3502.2	40.5	8354	18	US-10-029-020-13	Sequence 13, Appl1
22	3482.2	40.3	9826	9	US-09-808-602-77	Sequence 7, Appl1
23	3482.2	40.3	9826	10	US-09-800-198-7	Sequence 79, Appl1
24	3466.4	40.1	9695	17	US-10-144-194A-81	Sequence 81, Appl1
25	3466.4	40.1	9695	20	US-10-491-566-81	Sequence 81, Appl1
26	3453.8	40.0	9729	9	US-09-808-602-12	Sequence 12, Appl1
27	3453.8	40.0	9729	10	US-09-800-198-12	Sequence 12, Appl1
28	3439.2	39.8	8645	22	US-10-467-535-22	Sequence 22, Appl1
29	3264.8	37.8	9058	17	US-10-144-194A-79	Sequence 79, Appl1
30	3264.8	37.8	9058	20	US-10-491-566-79	Sequence 79, Appl1
31	3249.6	37.6	8355	17	US-10-383-201-55	Sequence 55, Appl1
32	3158	36.5	7781	20	US-10-723-860-2302	Sequence 2302, Ap
33	2854.8	33.0	8297	20	US-10-723-860-4101	Sequence 4101, Ap
34	2854.8	33.0	12880	17	US-10-295-027-927	Sequence 927, Ap
35	2670	30.9	6771	20	US-10-723-860-6509	Sequence 6509, Ap
36	2599	30.1	6560	9	US-09-808-602-76	Sequence 76, Appl1
37	2599	30.1	6560	10	US-09-800-198-64	Sequence 64, Appl1
38	1671.2	19.3	8624	20	US-10-723-860-3169	Sequence 3169, Ap
39	1671.2	19.3	8624	22	US-10-756-149-2959	Sequence 2959, Ap
40	1615.2	18.7	8774	20	US-10-723-860-7116	Sequence 7176, Ap
41	1580.6	18.3	4245	21	US-10-494-940-38	Sequence 74, Appl
42	1442	16.7	1534	20	US-10-128-558-121	Sequence 121, Appl
43	912.8	10.6	3217	14	US-10-198-846-13976	Sequence 13976, A
44	766.4	8.9	791	9	US-09-823-245A-85	Sequence 85, Appl1
45	706	8.2	2496	9	US-09-808-602-75	Sequence 75, Appl1

ALIGNMENTS

RESULT 1
US-10-038-854-37
Sequence 37, Application US/10038854
Publication No. US20040022781A1
GENERAL INFORMATION: Kimberly A
APPLICANT: Spytek, Kimberly A
APPLICANT: Li, Li
APPLICANT: Wolenc, Adam R
APPLICANT: Verneet, Corine
APPLICANT: Eissen, Andrew J
APPLICANT: Liu, Xiaohong
APPLICANT: Waiyanhar, Urie M
APPLICANT: Shinkets, Richard A
APPLICANT: Tchervet, Velizar
APPLICANT: Spaderna, Steven K
APPLICANT: Gorman, Linda
APPLICANT: Kekuda, Ramesh
APPLICANT: Paturajan, Meera
APPLICANT: Gueev, Vladimiro Y
APPLICANT: Gangolli, Esna A
APPLICANT: Guo, Xiaojia S
APPLICANT: Shenoy, Suresh G
APPLICANT: Rastelli, Luca
APPLICANT: Casman, Seacie J
APPLICANT: Boldog, Ferenc
APPLICANT: Burgess, Catherine E
APPLICANT: Edinger, Shlomit R
APPLICANT: Killeman, Karen
APPLICANT: Gunther, Erik
APPLICANT: Smithson, Glenda

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OM nucleic - nucleic search, using sw model

Run on: September 26, 2005, 22:25:30 / Search time 892 Seconds
(without alignments)
15858.310 Million cell updates/sec

Title: US-10-038-854-37

Perfect score: 8645
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	709.4	8.2	2007	4	US-09-976-594-407
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3	345.8	4.0	3111	4	US-09-514-573-1
4	345.4	4.0	1680	3	US-08-891-845-3
5	345.4	4.0	1680	4	US-09-514-573-3
6	267.8	3.1	2387	3	US-08-891-845-11
7	267.8	3.1	2387	4	US-09-514-573-11
8	112.4	1.3	288	4	US-09-513-999C-23277
9	74.6	0.9	6049	4	US-08-793-273C-3
10	74.6	0.9	6049	5	PCT-US95-11684-3
11	72.2	0.8	3033	4	US-09-724-797-81
12	70	0.8	1515	4	US-09-902-540-9184
C 13	70	0.8	9556	4	US-09-902-540-982
C 14	69.6	0.8	28509	4	US-09-902-540-1240
15	68.6	0.8	6763	4	US-09-949-016-3399
16	68.6	0.8	13857	4	US-09-620-312D-75
17	68.6	0.8	34534	4	US-09-949-016-15141
18	68.4	0.8	2244	4	US-09-902-540-9009
19	68.4	0.8	12849	4	US-09-902-540-963
20	68.4	0.8	47981	4	US-09-679-279-1
21	68.2	0.8	2277	1	US-08-676-974-5
22	68.2	0.8	2277	2	US-09-098-487-5
23	68.2	0.8	1260	4	US-09-902-540-8673
24	67	0.8	9191	4	US-09-902-540-918
C 25	66.6	0.8	7286	4	US-08-793-273C-1
26	66.6	0.8	7286	5	PCT-US95-11684-1
27	66.6	0.8	7286	5	PCT-US95-11684-1

28	65.6	0.8	1104	4	US-09-902-540-9182	Sequence 9182, Ap
29	65.6	0.8	1836	4	US-09-266-965-52	Sequence 52, Appl
30	65.6	0.8	53500	4	US-09-266-965-52	Sequence 76, Appl
C 31	65.4	0.8	2862	4	US-09-252-991A-10659	Sequence 10659, A
32	65.4	0.8	2910	4	US-09-252-991A-10414	Sequence 10414, A
33	65.4	0.8	3111	4	US-09-252-991A-10504	Sequence 10504, A
C 34	64.8	0.7	601	4	US-09-949-016-121670	Sequence 121670, A
35	64.6	0.7	1158	4	US-09-902-540-3017	Sequence 3017, Ap
36	64.6	0.7	3733	4	US-09-902-540-639	Sequence 639, App
C 37	64.4	0.7	601	4	US-09-949-016-121669	Sequence 121669, A
38	63.8	0.7	50341	1	US-08-247-901C-1	Sequence 1, Appl1
39	63.8	0.7	50341	2	US-09-075-904-1	Sequence 1, Appl1
40	63.8	0.7	52297	3	US-09-426-436-1	Sequence 1, Appl1
41	63.8	0.7	52297	3	US-08-705-557-1	Sequence 1, Appl1
42	63.6	0.7	2061	4	US-09-252-991A-1544	Sequence 1544, Ap
43	63.6	0.7	4319	4	US-09-475-515-6	Sequence 6, Appl1
44	63.6	0.7	41170	4	US-09-902-540-1267	Sequence 1267, Ap
45	62.8	0.7	4403765	3	US-09-103-840A-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-09-976-594-407/C
Sequence 407, Application US/09976594
Patent No. 6673549
GENERAL INFORMATION:
APPLICANT: Buchinder, Jenny
TITLE OR INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
SEQ ID NO 407
LENGTH: 2007
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673549 474200.1
US-09-976-594-407
Query Match 8.2%; Score 709.4; DB 4; Length 2007;
Best Local Similarity 99.6%; Pred. No. 6.5e-175;
Matches 732; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
C 7913 GCGGCCGCAAGCGCTGAGAGCGCATCAACGTGACGTGTGCGACATCCACCAAGGTGG 7972
2007 GCGGCCGCAAGCGCTGAGAGCGCATCAACGTGACGTGTGCGACATCCACCAAGGTGG 1948
7973 TGAACGCGAGAGCGCGAGGTTGCGGAGCGTGAAGATGCAAGTTGCGCGCTGCGCTG- 8031
1947 TGAATCGCAGAGAGCGCGAGGTTGCGGAGCGTGAAGATGCAAGTTGCGCGCTGCGCTG- 1888
8032 CACGTGCGCTACGCGATGACATCCCTTGAGAG-AGGAGAAAGCGCGCATCTCTGAGAGGCGCG 8090
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8151 GCGCGCGCGCTGCGCGCGCGCGAGAGGCGCGAGCGCGCTGCGCGCGCGAGAGGTTGCA 8210
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8211 GCGCGCGCGCTGCGCGCGCGCGAGAGGCGCGAGCGCGCTGCGCGCGCGAGAGGTTGCA 8270

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OM nucleic - nucleic search, using sw model

Run on: September 26, 2005, 18:17:29 ; Search time 2727 Seconds
(without alignments)
18766.470 Million cell updates/sec

Title: US-10-038-854-37

Perfect score: 8645
Sequence: 1 ttctgctcggccagaatt.....actgtattactacttta 8645

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: Geneseq2003bs.*
10: Geneseq2003cs.*
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12: Geneseq2004bs.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	8616.6	99.7	8657	12	ADH41932 Novel hum
4	8615	99.7	8657	12	ADH41990 Novel hum
5	8615	99.7	8657	12	ADH41992 Novel hum
6	8615	99.7	8657	12	ADH41994 Novel hum
7	8615	99.7	8657	12	ADH41996 Novel hum
8	8613.8	99.6	8675	6	ABQ82343 Human NOV
9	8594	99.4	8636	12	ADH41998 Novel hum
10	8163.6	99.4	8204	12	ADH41972 Novel hum
11	8000.6	99.5	8473	12	ADH41948 Novel hum
12	7997.8	92.5	8473	6	ABQ82345 Human NOV
13	7895.8	91.3	8487	12	ADH41976 Novel hum
14	7893.6	91.3	8487	6	ABQ82346 Human NOV
15	6789.2	78.5	8964	12	ADH01384 Teneurin
16	5952.8	68.9	6810	12	ADQ025481 Human sof
17	5305.8	61.4	5309	12	ADQ021673 Human sof
18	3714.8	43.0	8575	6	AD116607 Human NOV
19	3714.8	43.0	8575	12	ADH71271 Human gen
20	3614	41.8	3614	4	AAH14183 Human CDN

21	3614	41.8	3614	13	ADR25882	Ad25882 Breast ca
22	3589.8	41.5	8438	6	ABN85378	ABN85378 Human NOV
23	3572.8	41.3	9852	12	ADH71219	Adh71219 Human gen
24	3545.6	41.0	8797	12	ADJ75919	Adj75919 Marker ge
25	3502.2	40.5	8354	6	AB552100	AB552100 Human TEN
26	3502.2	40.5	8354	10	ADPF4829	Adpf4829 Murine NO
27	3482.2	40.3	9668	12	ADH71239	Adh71239 Human gen
28	3482.2	40.3	9756	12	ADH71249	Adh71249 Human gen
29	3482.2	40.3	9823	12	ADH71257	Adh71257 Human gen
30	3482.2	40.3	9823	12	ADH71245	Adh71245 Human gen
31	3482.2	40.3	9826	5	AA514085	AA514085 Human FCT
32	3482.2	40.3	9826	12	ADH71253	Adh71253 Human gen
33	3466.4	40.1	9695	8	ACC72052	Acc72052 BCY0205B
34	3460.8	40.0	9826	10	ADB32023	Adb32023 Human FCT
35	3455.8	40.0	9729	5	AA514089	AA514089 Human FCT
36	3453.8	40.0	9729	10	ADB32028	Adb32028 Human FCT
37	3453.8	40.0	9729	12	ADH71251	Adh71251 Human gen
38	3439.2	39.8	8645	6	AB578652	Ab578652 Human CDN
39	3423.2	39.6	8574	12	ADN42261	Adh71227 Human gen
40	3392	39.2	6999	12	ADH71273	Adh71273 Human gen
41	3270	37.8	3270	4	AAH14671	AAH14671 Human CDN
42	3264.8	37.6	9058	8	ACC72051	Acc72051 BCY0205A
43	3249.6	37.6	8355	10	ADPF4841	Adpf4841 Murine NO
44	3158	36.5	7781	12	ADQ19483	Adq19483 Human sof
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ALIGNMENTS

RESULT 1	
ID	ADH41968 standard; DNA; 8645 BP.
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AC	ADH41968;
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DT	25-MAR-2004 (first entry)
XX	
DE	Novel human nucleic acid NOV408.
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KW	anorectic; antidiabetic; immunosuppressive; anti-HIV; neuroprotective;
KW	nootropic; antiparkinsonian; antiasclmatic; antifertility;
KW	cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes;
KW	AIDS; multiple sclerosis; graft-versus-host disease; Alzheimer's disease;
KW	Parkinson's disease; asthma; fertility disorder; chromosome mapping;
KW	tissue typing; preventive medicine; pharmacogenomic; vaccine.
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OS	Homo sapiens.
XX	
PN	WC0003102159-A2.
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PD	11-DEC-2003.
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PF	04-JUN-2003; 2003WO-US017573.
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PR	04-JUN-2002; 2002US-0385490P.
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PR	04-JUN-2002; 2002US-0385615P.
XX	
PR	04-JUN-2002; 2002US-0385755P.
XX	
PR	05-JUN-2002; 2002US-0386041P.
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PR	06-JUN-2002; 2002US-0386355P.
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PR	07-JUN-2002; 2002US-0386701P.
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PR	10-JUN-2002; 2002US-0387429P.

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17617.670 Million cell updates/sec

Title: US-10-038-854-37

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Searched: 4708233 seqs, 24227607955 residues

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 13: gb_un:*
- 14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	8000.6	92.5	8473	6	AX662357 Sequence
4	7895.8	91.3	8487	6	AX662359 Sequence
5	6789.2	78.5	8964	6	AX952856 Sequence
6	6789.2	78.5	8964	10	AB025412 Mus muscu
7	6270	72.5	6751	6	CQ716754 Sequence
8	5749.4	66.5	7816	10	AF195418 Mus muscu
9	5305.8	61.4	5309	9	AB040888 Homo sap1
10	4561.4	52.8	5804	10	AK122513 Mus muscu
11	4273.8	49.4	8816	5	AB026978 Danio rer
12	3714.8	43.0	8575	6	AX921803 Sequence
13	3614	41.8	3614	6	BD156175 Primer fo
14	3614	41.8	3614	6	AX876525 Sequence
15	3589.8	41.5	8438	6	AX001336 Homo sap1
16	3589.8	41.5	8438	6	AX675551 Sequence
17	3566.6	41.3	8409	6	GA279031 Gallus ga
18	3566.6	41.3	8409	6	AX250068 Sequence
19	3545.6	41.0	8797	6	CQ777485 Sequence

20	3545.6	41.0	8797	6	AX250063
21	3545.6	41.0	8797	6	AX250066 Sequence
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23	3518.4	40.7	8689	6	AX250067 Sequence
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25	3502.2	40.5	8354	6	AX556500 Sequence
26	3482.2	40.3	9826	6	AX250008 Sequence
27	3453.8	40.0	9729	6	AX250013 Sequence
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29	3439.2	39.8	8645	6	AX600210 Sequence
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31	3270	37.8	3270	9	AX877449 Sequence
32	3270	37.8	3270	6	AK001748 Homo sap1
33	3267.6	37.8	9722	10	AF059485 Mus muscu
34	3235.6	37.4	3394	9	AK125869 Homo sap1
35	3182.4	36.8	7400	6	CQ727408 Sequence
36	3158	36.5	7781	9	AB032953 Sequence
37	3066.4	35.5	9264	5	AB026980 Danio rer
38	3012.6	34.8	8118	5	GA238613 Gallus ga
39	2991.8	34.6	8373	10	AB025410 Mus muscu
40	2970.8	34.4	7713	9	HSN808325 Homo sap1
41	2944.6	34.1	7514	6	CQ722991 Sequence
42	2872.4	33.2	7706	6	CQ714850 Sequence
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44	2599	30.1	6560	6	AX250065 Sequence
45	2155.4	24.9	2157	6	BD156088 Primer fo

ALIGNMENTS

RESULT 1	AX662355	8645 bp	DNA	linear	PAT 22-MAR-2003
LOCUS	AX662355	Sequence 37 from Patent WO02062999.			
DEFINITION	AX662355				
ACCESSION	AX662355				
VERSION	AX662355.1	GI:29163217			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE					
AUTHORS	Spytek, K.A., Li, L., Wolenc, A.R., Vernet, C.A., Eisen, A., Liu, X., Malyankar, U., Shinkov, R.A., Tcherny, V.T., Spaderna, S.K., Gorman, L., Kerkuta, R., Patturajan, M., Gusev, V., Gangoli, B.A., Guo, X., Shenoy, S., Raselli, L., Casman, S.J., Boldog, F., Burgess, C.B., Edinger, S., Eilerman, K., Gunther, B., Smithson, G., Milet, I. and Nucleic acids encoding same				
TITLE	Protein and nucleic acids encoding same				
JOURNAL	Patent: WO 02062999-A 37 15-AUG-2002; Curagen Corporation (US)				
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	/mol_type="unassigned DNA"				
	/db_xref="taxon:9606"				
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Best Local Similarity	100.0%; Pred. NO. 0;				
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DB	1 TTGGCTTCGGGCGCAAGTATGGCGAGGGGCTTGAGCTTGAGGAGAGCTGAAGT	60			
QY	61 AAGGATTAACCTTAAGAGAGGCCAATGAAGCTTGAACCTGAAGCTTGAACAGCA	120			
DB	61 AAGGATTAACCTTAAGAGAGGCCAATGAAGCTTGAACCTGAAGCTTGAAGCTTGA	120			
QY	121 GGACGATGTGACACAGAGAGAGAGTATGATGTGAAGAGACGACGCTTACTGC	180			